==
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2009; month=4; day=13; hr=17; min=2; sec=7; ms=359;]
==

Application No: 10566409   Version No: 2.0

Input Set:

Output Set:

Started: 2009-03-20 18:24:37.386
Finished: 2009-03-20 18:24:55.179
Elapsed: 0 hr(s) 0 min(s) 17 sec(s) 793 ms
Total Warnings: 631
Total Errors: 9
No. of SeqIDs Defined: 699
Actual SeqID Count: 699

Error code   Error Description

W   213   Artificial or Unknown found in <213>   in SEQ ID (19)

W   213   Artificial or Unknown found in <213>   in SEQ ID (20)

W   213   Artificial or Unknown found in <213>   in SEQ ID (27)

W   213   Artificial or Unknown found in <213>   in SEQ ID (28)

W   213   Artificial or Unknown found in <213>   in SEQ ID (29)

W   213   Artificial or Unknown found in <213>   in SEQ ID (30)

W   213   Artificial or Unknown found in <213>   in SEQ ID (31)

W   213   Artificial or Unknown found in <213>   in SEQ ID (32)

W   213   Artificial or Unknown found in <213>   in SEQ ID (33)

W   213   Artificial or Unknown found in <213>   in SEQ ID (34)

W   213   Artificial or Unknown found in <213>   in SEQ ID (35)

W   213   Artificial or Unknown found in <213>   in SEQ ID (36)

W   213   Artificial or Unknown found in <213>   in SEQ ID (37)

W   213   Artificial or Unknown found in <213>   in SEQ ID (38)

W   213   Artificial or Unknown found in <213>   in SEQ ID (39)

W   213   Artificial or Unknown found in <213>   in SEQ ID (40)

W   213   Artificial or Unknown found in <213>   in SEQ ID (41)

W   213   Artificial or Unknown found in <213>   in SEQ ID (42)

W   213   Artificial or Unknown found in <213>   in SEQ ID (43)

W   213   Artificial or Unknown found in <213>   in SEQ ID (44)

Input Set:

Output Set:

Started:	2009-03-20 18:24:37.386
Finished:	2009-03-20 18:24:55.179
Elapsed:	0 hr(s) 0 min(s) 17 sec(s) 793 ms
Total Warnings:	631
Total Errors:	9
No. of SeqIDs Defined:	699
Actual SeqID Count:	699

Error code	Error Description
	This error has occured more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (201)
W 402	Undefined organism found in <213> in SEQ ID (202)
W 402	Undefined organism found in <213> in SEQ ID (203)
W 402	Undefined organism found in <213> in SEQ ID (204)
W 402	Undefined organism found in <213> in SEQ ID (205)
W 402	Undefined organism found in <213> in SEQ ID (206)
E 257	Invalid sequence data feature in <221> in SEQ ID (212)
E 257	Invalid sequence data feature in <221> in SEQ ID (216)
W 402	Undefined organism found in <213> in SEQ ID (451)
W 402	Undefined organism found in <213> in SEQ ID (452)
W 402	Undefined organism found in <213> in SEQ ID (457)
W 402	Undefined organism found in <213> in SEQ ID (458)
W 251	Found intentionally skipped sequence in SEQID (520)
W 251	Found intentionally skipped sequence in SEQID (521)
W 251	Found intentionally skipped sequence in SEQID (522)
W 251	Found intentionally skipped sequence in SEQID (523)
W 251	Found intentionally skipped sequence in SEQID (524)
W 251	Found intentionally skipped sequence in SEQID (525)
W 251	Found intentionally skipped sequence in SEQID (526)
W 251	Found intentionally skipped sequence in SEQID (527)
W 251	Found intentionally skipped sequence in SEQID (639)

```
          Input Set:


          Output Set:



          Started:    2009-03-20 18:24:37.386
         Finished:    2009-03-20 18:24:55.179
          Elapsed:    0 hr(s) 0 min(s) 17 sec(s) 793 ms
   Total Warnings:    631
     Total Errors:    9
No. of SeqIDs Defined:  699
 Actual SeqID Count:    699
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Error code	Error Description
W 251	Found intentionally skipped sequence in SEQID (640)
W 251	Found intentionally skipped sequence in SEQID (643)
W 251	Found intentionally skipped sequence in SEQID (646)
W 251	Found intentionally skipped sequence in SEQID (680)
W 251	Found intentionally skipped sequence in SEQID (681)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
W 251	Found intentionally skipped sequence in SEQID (699)

<210> 1
<211> 714
<212> DNA
<213> Homo sapiens
<400> 1

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tctgatcagg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccagcacct     60
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga caccctcatg    120
atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga agaccctgag    180
gtcaagttca actggtacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg    240
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac    300
tggctgaatg gcaaggagta caagtgcaag gtctccaaca aagccctccc agcccccatc    360
gagaaaacaa tctccaaagc caaagggcag ccccgagaac cacaggtgta caccctgccc    420
ccatcccggg atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc    480
tatcccagcg acatcgccgt ggagtgggag agcaatgggc agccggagaa caactacaag    540
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gctcaccgtg    600
gacaagagca ggtggcagca ggggaacgtc ttctcatgct ccgtgatgca tgaggctctg    660
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gtaaatgatc taga          714
```

<210> 2
<211> 235
<212> PRT
<213> Homo sapiens
<400> 2

```
Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
1               5                   10                  15
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
            20                  25                  30
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
        35                  40                  45
```

```
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
    50                      55                  60
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
65                      70                  75                  80
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
                    85                  90                  95
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
                100                 105                 110
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
            115                 120                 125
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
    130                     135                 140
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
145                     150                 155                 160
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
                165                 170                 175
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
            180                 185                 190
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
        195                 200                 205
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
    210                     215                 220
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225                     230                 235
```

<210> 3
<211> 718
<212> DNA
<213> Lama glama
<220>
<221> modified_base
<222> (34)..(34)
<223> n is a, c, g, or t
<220>
<221> modified_base
<222> (43)..(43)
<223> n is a, c, g, or t
<220>
<221> modified_base
<222> (52)..(52)
<223> n is a, c, g, or t
<220>
<221> modified_base
<222> (55)..(55)
<223> n is a, c, g, or t
<220>
<221> modified_base
<222> (58)..(58)
<223> n is a, c, g, or t
<220>
<221> modified_base
<222> (64)..(64)
<223> n is a, c, g, or t
<400> 3
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tgatcaagaa ccacatggag gatgcacgtg cccncagtgc ccncaatgcc cngcnccnga      60
actnccagga ggcccttctg tctttgtctt cccccgaaa cccaaggacg tcctctccat      120
ttttggaggc cgagtcacgt gcgttgtagt ggacgtcgga aagaaagacc ccgaggtcaa      180
```

```
tttcaactgg tatattgatg gcgttgaggt gcgaacggcc aatacgaagc caaaagagga      240
acagttcaac agcacgtacc gcgtggtcag cgtcctgccc atccagcacc aggactggct      300
gacggggaag gaattcaagt gcaaggtcaa caacaaagct ctcccggccc ccatcgagag      360
gaccatctcc aaggccaaag ggcagacccg ggagccgcag gtgtacaccc tggccccaca      420
ccgggaagaa ctggccaagg acaccgtgag cgtaacatgc ctggtcaaag cttctacccc      480
agctgacatc aacgttgagt ggcagaggaa cggtcagccg gagtcagagg gcacctacgc      540
caacacgccg ccacagctgg acaacgacgg gacctacttc ctctacagca agctctcggt      600
gggaaagaac acgtggcagc ggggagaaac cttaacctgt gtggtgatgc atgaggccct      660
gcacaaccac tacacccaga atccatcacc cagtcttcg ggtaaatagt aatctaga      718
```

<210> 4
<211> 231
<212> PRT
<213> Lama glama
<400> 4

```
Glu Pro His Gly Gly Cys Thr Cys Pro Gln Cys Pro Ala Pro Glu Leu
1               5                   10                  15
Pro Gly Gly Pro Ser Val Phe Val Phe Pro Pro Lys Pro Lys Asp Val
            20                  25                  30
Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val Asp Val
        35                  40                  45
Gly Lys Glu Asp Pro Glu Val Asn Phe Asn Trp Tyr Ile Asp Gly Val
    50                  55                  60
Glu Val Arg Thr Ala Asn Thr Lys Pro Lys Glu Glu Gln Phe Asn Ser
65                  70                  75                  80
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp Leu
                85                  90                  95
Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ala
            100                 105                 110
Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu Pro
        115                 120                 125
Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp Thr
    130                 135                 140
Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Ala Asp Ile Asn
145                 150                 155                 160
Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr Ala
                165                 170                 175
Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr Ser
            180                 185                 190
Arg Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr Leu Thr
        195                 200                 205
Gly Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
    210                 215                 220
Ile Thr Gln Ser Ser Gly Lys
225                 230
```

<210> 5
<211> 757
<212> DNA
<213> Lama glama
<400> 5

```
tgatcaagaa cccaagacac caaaaccaca accacaacca caaccacaac ccaatcctac       60
aacagaatcc aagtgtccca aatgtccagc ccctgagctc ctgggagggc cctcagtctt      120
catcttcccc ccgaaaccca aggacgtcct ctccatttct gggaggcccg aggtcacgtg      180
cgttgtggta gacgtgggcc aggaagaccc cgaggtcagt ttcaactggt acattgatgg      240
cgctgaggtg cgaacggcca acacgaggcc aaaagaggaa cagttcaaca gcacgtaccg      300
cgtggtcagc gtcctgccca tccagcacca ggactggctg acggggaagg aattcaagtg      360
```

```
         caaggtcaac aacaaagctc tcccggcccc catcgagaag accatctcca aggccaaagg      420
         gcagacccgg gagccgcagg tgtacaccct ggccccacac cgggaagagc tggccaagga      480
         caccgtgagc gtaacatgcc tggtcaaagg cttctaccca cctgatatca cgttgagtg       540
         gcagaggaat gggcagccgg agtcagaggg cacytacgcc accacgccac cccagctgga      600
         caacgacggg acctacttcc tctacagcaa gctctcggtg ggaaagaaca cgtggcagca      660
         gggagaaacc ttcacctgtg tggtgatgca cgaggccctg cacaaccact acacccagaa      720
         atccatcacc cagtcttcgg gtaaatagta atctaga                               757


    <210> 6
    <211> 248
    <212> PRT
    <213> Lama glama
    <400> 6
         Asp Gln Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln
         1               5                   10                  15
         Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu
                     20                  25                  30
         Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
                 35                  40                  45
         Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val Asp
             50                  55                  60
         Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly
         65                  70                  75                  80
         Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn
                     85                  90                  95
         Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp
                     100                 105                 110
         Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro
                 115                 120                 125
         Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu
             130                 135                 140
         Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp
         145                 150                 155                 160
         Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile
                     165                 170                 175
         Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr
                     180                 185                 190
         Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr
                 195                 200                 205
         Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe
             210                 215                 220
         Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
         225                 230                 235                 240
         Ser Ile Thr Gln Ser Ser Gly Lys
                         245


    <210> 7
    <211> 727
    <212> DNA
    <213> Lama glama
    <400> 7
         tgatcaagcg caccacagcg aagaccccag ctccaagtgt cccaaatgcc caggccctga       60
         actccttgga gggcccacgg tcttcatctt cccccgaaa gccaaggacg tcctctccat       120
         cacccgaaaa cctgaggtca cgtgcttgtg gtggacgtgg taaagaaga ccctgagatc       180
         gagttcaagc tggtccgtgg atgacacaga ggtacacacg gctgagacaa agccaaagga      240
         ggaacagttc aacagcacgt accgcgtggt cagcgtcctg cccatccagc accaggactg      300
         gctgacgggg aaggaattca gtgcaaggt caacaacaaa gctctcccag cccccatcga      360
```

```
      gaggaccatc tccaaggcca aagggcagac ccgggagccg caggtgtaca ccctggcccc      420
      acaccgggaa gagctggcca aggacaccgt gagcgtaacc tgcctggtca aaggcttctt      480
      cccagctgac atcaacgttg agtggcagag gaatgggcag ccggagtcag agggcaccta      540
      cgccaacacg ccgccacagc tggacaacga cgggacctac ttcctctaca gcaaactctc      600
      cgtgggaaag aacacgtggc agcagggaga agtcttcacc tgtgtggtga tgcacgaggc      660
      tctacacaat cactccaccc agaaatccat cacccagtct tcgggtaaat agtaatctag      720
      agggccc                                                                727
```

<210> 8
<211> 236
<212> PRT
<213> Lama glama
<400> 8

```
      Asp Gln Ala His His Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys
      1               5                   10                  15
      Pro Gly Pro Glu Leu Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro
                  20                  25                  30
      Lys Ala Lys Asp Val Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys
                  35                  40                  45
      Leu Trp Trp Thr Trp Val Lys Lys Thr Leu Arg Ser Ser Ser Ser Trp
          50                  55                  60
      Ser Val Asp Asp Thr Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu
      65                  70                  75                  80
      Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln
                          85                  90                  95
      His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
                  100                 105                 110
      Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly
                  115                 120                 125
      Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu
          130                 135                 140
      Leu Ala Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe
      145                 150                 155                 160
      Pro Ala Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser
                          165                 170                 175
      Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr
                  180                 185                 190
      Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln
          195                 200                 205
      Gly Glu Val Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His
          210                 215                 220
      Ser Thr Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
      225                 230                 235
```

<210> 9
<211> 54
<212> DNA
<213> Homo sapiens
<400> 9

```
      gatcaggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agca           54
```

<210> 10
<211> 18
<212> PRT
<213> Homo sapiens
<400> 10

```
      Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
```

```
        1               5                   10                  15
        Pro Ala


<210> 11
<211> 54
<212> DNA
<213> Homo sapiens
<400> 11
        gatctggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agca          54


<210> 12
<211> 18
<212> PRT
<213> Homo sapiens
<400> 12
        Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
        1               5                   10                  15
        Pro Ala


<210> 13
<211> 327
<212> DNA
<213> Homo sapiens
<400> 13
        cctgaactcc tggggggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc     60
        atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct    120
        gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg    180
        cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag    240
        gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc    300
        atcgagaaaa ccatctccaa agccaaa                                        327


<210> 14
<211> 109
<212> PRT
<213> Homo sapiens
<400> 14
        Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
        1               5                   10                  15
        Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
                    20                  25                  30
        Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                35                  40                  45
        Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
            50                  55                  60
        Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
        65                  70                  75                  80
        Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                        85                  90                  95
        Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
                    100                 105


<210> 15
<211> 324
<212> DNA
<213> Homo sapiens
<400> 15
        gggcagcccc gagaaccaca ggtgtacacc ctgcccccat cccgggagga gatgaccaag     60
```

```
     aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag        120
     tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc        180
     gacggctcct tcttcctcta tagcaagctc accgtggaca gagcaggtg gcagcagggg         240
     aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc        300
     ctctccctgt ccccgggtaa atga                                               324


<210> 16
<211> 107
<212> PRT
<213> Homo sapiens
<400> 16
     Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
     1               5                   10                  15
     Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                     20                  25                  30
     Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
             35                  40                  45
     Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
         50                  55                  60
     Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
     65                  70                  75                  80
     Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
                     85                  90                  95
     Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                     100                 105


<210> 17
<211> 54
<212> DNA
<213> Homo sapiens
<400> 17
     gatcaggagc ccaaatcttc tgacaaaact cacacatccc caccgtcccc agca             54


<210> 18
<211> 18
<212> PRT
<213> Homo sapiens
<400> 18
     Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser
     1               5                   10                  15
     Pro Ala


<210> 19
<211> 712
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Synthetic
     nucleotide sequence
<400> 19
     tgatcacccc aaatcttctg acaaaactca cacatctcca ccgtcctcag cacctgaact        60
     cctgggtgga ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc        120
     ccggacccct gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa        180
     gttcaactgg tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga        240
```